

Raw Sequence Listing Error Summary

ERROR DETECTED

SUGGESTED CORRECTION

SERIAL NUMBER:

09/773,977

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE

1 _____ Wrapped Nucleics
_____ Wrapped Aminos

The number/text at the end of each line "wrapped" down to the next line. This may occur if your file was retrieved in a word processor after creating it. Please adjust your right margin to .3; this will prevent "wrapping."

2 _____ Invalid Line Length

The rules require that a line not exceed 72 characters in length. This includes white spaces.

3 _____ Misaligned Amino
_____ Numbering

The numbering under each 5th amino acid is misaligned. Do not use tab codes between numbers; use space characters, instead.

4 _____ Non-ASCII

The submitted file was not saved in ASCII(DOS) text, as required by the Sequence Rules. Please ensure your subsequent submission is saved in ASCII text.

5 _____ Variable Length

Sequence(s) _____ contain n's or Xaa's representing more than one residue. Per Sequence Rules, each n or Xaa can only represent a single residue. Please present the maximum number of each residue having variable length and indicate in the <220>-<223> section that some may be missing.

6 _____ PatentIn 2.0
_____ "bug"

A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid sequences(s) _____. Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence. This applies to the mandatory <220>-<223> sections for Artificial or Unknown sequences.

7 _____ Skipped Sequences
_____ (OLD RULES)

Sequence(s) _____ missing. If intentional, please insert the following lines for each skipped sequence:
(2) INFORMATION FOR SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
(i) SEQUENCE CHARACTERISTICS: (Do not insert any subheadings under this heading)
(xi) SEQUENCE DESCRIPTION:SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
This sequence is intentionally skipped

Please also adjust the "(ii) NUMBER OF SEQUENCES:" response to include the skipped sequences.

8 _____ Skipped Sequences
_____ (NEW RULES)

Sequence(s) _____ missing. If intentional, please insert the following lines for each skipped sequence.
<210> sequence id number
<400> sequence id number
000

9 _____ Use of n's or Xaa's
_____ (NEW RULES)

Use of n's and/or Xaa's have been detected in the Sequence Listing.
Per 1.823 of Sequence Rules, use of <220>-<223> is MANDATORY if n's or Xaa's are present.
In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.

10 _____ Invalid <213>
_____ Response

Per 1.823 of Sequence Rules, the only valid <213> responses are: Unknown, Artificial Sequence, or scientific name (Genus/species). <220>-<223> section is required when <213> response is Unknown or is Artificial Sequence

11 ✓ _____ Use of <220>

Sequence(s) _____ missing the <220> "Feature" and associated numeric identifiers and responses. Use of <220> to <223> is MANDATORY if <213> "Organism" response is "Artificial Sequence" or "Unknown." Please explain source of genetic material in <220> to <223> section.
(See "Federal Register," 06/01/1998, Vol. 63, No. 104, pp. 29631-32) (Sec. 1.823 of Sequence Rules)

12 _____ PatentIn 2.0
_____ "bug"

Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing). Instead, please use "File Manager" or any other manual means to copy file to floppy disk.

13 _____ Misuse of n

n can only be used to represent a single nucleotide in a nucleic acid sequence. N is not used to represent any value not specifically a nucleotide.

AMC/MH - Biotechnology Systems Branch - 08/21/2001

The types of errors shown exist throughout the Sequence Listing. Please check subsequent sequences for similar errors.

OIPE

RAW SEQUENCE LISTING

DATE: 08/07/2001

PATENT APPLICATION: US/09/773,877

TIME: 08:23:37

Input Set : A:\REG 710B.txt

Output Set: N:\CRF3\08072001\I773877.raw

3 <110> APPLICANT: Xia, Yu-Ping et al.
 5 <120> TITLE OF INVENTION: METHODS FOR TREATING INFLAMMATORY SKIN DISEASES
 7 <130> FILE REFERENCE: REG 710b
 9 <140> CURRENT APPLICATION NUMBER: 09/773,877
 10 <141> CURRENT FILING DATE: 2001-01-31
 12 <160> NUMBER OF SEQ ID NOS: 27
 14 <170> SOFTWARE: PatentIn version 3.0
 16 <210> SEQ ID NO: 1
 17 <211> LENGTH: 36
 18 <212> TYPE: DNA
 C--> 19 <213> ORGANISM: Artificial ✓
 21 <220> FEATURE:
 22 <223> OTHER INFORMATION: Primer ✓
 24 <400> SEQUENCE: 1
 25 gactagcagt ccggaggttag accttttcgta gagatg 36
 28 <210> SEQ ID NO: 2
 29 <211> LENGTH: 33
 30 <212> TYPE: DNA
 C--> 31 <213> ORGANISM: Artificial ✓
 33 <220> FEATURE:
 34 <223> OTHER INFORMATION: Primer ✓
 36 <400> SEQUENCE: 2
 37 cggactcaga accacatcta tgattgtatt ggt 33
 40 <210> SEQ ID NO: 3
 41 <211> LENGTH: 35
 42 <212> TYPE: DNA
 C--> 43 <213> ORGANISM: Artificial ✓
 45 <220> FEATURE:
 46 <223> OTHER INFORMATION: Primer ✓
 48 <400> SEQUENCE: 3
 49 acaatcatag atgtggttct gagtccgtct catgg 35
 52 <210> SEQ ID NO: 4
 53 <211> LENGTH: 38
 54 <212> TYPE: DNA
 C--> 55 <213> ORGANISM: Artificial ✓
 57 <220> FEATURE:
 58 <223> OTHER INFORMATION: Primer ✓
 60 <400> SEQUENCE: 4
 61 gataatgccg gggccctttt catggaccct gacaaatg 38
 64 <210> SEQ ID NO: 5
 65 <211> LENGTH: 36
 66 <212> TYPE: DNA
 C--> 67 <213> ORGANISM: Artificial
 69 <220> FEATURE:
 70 <223> OTHER INFORMATION: Primer
 72 <400> SEQUENCE: 5
 73 gactagcagt ccggaggttag accttttcgta gagatg 36

PS

Does Not Comply
Corrected Diskette Needed

RAW SEQUENCE LISTING

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DATE: 08/07/2001

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Input Set : A:\REG 710B.txt

Output Set: N:\CRF3\08072001\I773877.raw

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76 <210> SEQ ID NO: 6
77 <211> LENGTH: 38
78 <212> TYPE: DNA
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81 <220> FEATURE:
82 <223> OTHER INFORMATION: Primer
84 <400> SEQUENCE: 6
85 ttcctgggca acagctggat atctatgatt gtattggt 38
88 <210> SEQ ID NO: 7
89 <211> LENGTH: 39
90 <212> TYPE: DNA
C--> 91 <213> ORGANISM: Artificial
93 <220> FEATURE:
94 <223> OTHER INFORMATION: Primer
96 <400> SEQUENCE: 7
97 atccagctgt tgcccaggaa gtcgctggag ctgctggta 39
100 <210> SEQ ID NO: 8
101 <211> LENGTH: 39
102 <212> TYPE: DNA
C--> 103 <213> ORGANISM: Artificial
105 <220> FEATURE:
106 <223> OTHER INFORMATION: Primer
108 <400> SEQUENCE: 8
109 attttcatgc acaatgacct cgggtgctctc ccgaaatcg 39
112 <210> SEQ ID NO: 9
113 <211> LENGTH: 38
114 <212> TYPE: DNA
C--> 115 <213> ORGANISM: Artificial
117 <220> FEATURE:
118 <223> OTHER INFORMATION: Primer
120 <400> SEQUENCE: 9
121 tcatagatat ccagctgttg cccaggaagt cgctggag 38
124 <210> SEQ ID NO: 10
125 <211> LENGTH: 39
126 <212> TYPE: DNA
C--> 127 <213> ORGANISM: Artificial
129 <220> FEATURE:
130 <223> OTHER INFORMATION: Primer
132 <400> SEQUENCE: 10
133 gataatgccg gggccatttt catgcacaat gacctcgg 39
136 <210> SEQ ID NO: 11
137 <211> LENGTH: 1704
138 <212> TYPE: DNA
C--> 139 <213> ORGANISM: Artificial
141 <220> FEATURE:
142 <223> OTHER INFORMATION: Flt1(1-3)-Fc
144 <220> FEATURE:
145 <221> NAME/KEY: CDS
146 <222> LOCATION: (1)..(1704)

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Input Set : A:\REG 710B.txt

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148 <400> SEQUENCE: 11
149 atg gtc agc tac tgg gac acc ggg gtc ctg ctg tgc gcg ctg ctc agc      48
150 Met Val Ser Tyr Trp Asp Thr Gly Val Leu Leu Cys Ala Leu Leu Ser
151 1          5          10          15
153 tgt ctg ctt ctc aca gga tct agt tca ggt tca aaa tta aaa gat cct      96
154 Cys Leu Leu Leu Thr Gly Ser Ser Ser Gly Ser Lys Leu Lys Asp Pro
155          20          25          30
157 gaa ctg agt tta aaa ggc acc cag cac atc atg caa gca ggc cag aca      144
158 Glu Leu Ser Leu Lys Gly Thr Gln His Ile Met Gln Ala Gly Gln Thr
159          35          40          45
161 ctg cat ctc caa tgc agg ggg gaa gca gcc cat aaa tgg tct ttg cct      192
162 Leu His Leu Gln Cys Arg Gly Glu Ala Ala His Lys Trp Ser Leu Pro
163          50          55          60
165 gaa atg gtg agt aag gaa agc gaa agg ctg agc ata act aaa tct gcc      240
166 Glu Met Val Ser Lys Glu Ser Glu Arg Leu Ser Ile Thr Lys Ser Ala
167 65          70          75          80
169 tgt gga aga aat ggc aaa caa ttc tgc agt act tta acc ttg aac aca      288
170 Cys Gly Arg Asn Gly Lys Gln Phe Cys Ser Thr Leu Thr Leu Asn Thr
171          85          90          95
173 gct caa gca aac cac act ggc ttc tac agc tgc aaa tat cta gct gta      336
174 Ala Gln Ala Asn His Thr Gly Phe Tyr Ser Cys Lys Tyr Leu Ala Val
175          100          105          110
177 cct act tca aag aag aag gaa aca gaa tct gca atc tat ata ttt att      384
178 Pro Thr Ser Lys Lys Lys Glu Thr Glu Ser Ala Ile Tyr Ile Phe Ile
179          115          120          125
181 agt gat aca ggt aga cct ttc gta gag atg tac agt gaa atc ccc gaa      432
182 Ser Asp Thr Gly Arg Pro Phe Val Glu Met Tyr Ser Glu Ile Pro Glu
183          130          135          140
185 att ata cac atg act gaa gga agg gag ctc gtc att ccc tgc cgg gtt      480
186 Ile Ile His Met Thr Glu Gly Arg Glu Leu Val Ile Pro Cys Arg Val
187 145          150          155          160
189 acg tca cct aac atc act gtt act tta aaa aag ttt cca ctt gac act      528
190 Thr Ser Pro Asn Ile Thr Val Thr Leu Lys Lys Phe Pro Leu Asp Thr
191          165          170          175
193 ttg atc cct gat gga aaa cgc ata atc tgg gac agt aga aag ggc ttc      576
194 Leu Ile Pro Asp Gly Lys Arg Ile Ile Trp Asp Ser Arg Lys Gly Phe
195          180          185          190
197 atc ata tca aat gca acg tac aaa gaa ata ggg ctt ctg acc tgt gaa      624
198 Ile Ile Ser Asn Ala Thr Tyr Lys Glu Ile Gly Leu Leu Thr Cys Glu
199          195          200          205
201 gca aca gtc aat ggg cat ttg tat aag aca aac tat ctc aca cat cga      672
202 Ala Thr Val Asn Gly His Leu Tyr Lys Thr Asn Tyr Leu Thr His Arg
203          210          215          220
205 caa acc aat aca atc ata gat gtc caa ata agc aca cca cgc cca gtc      720
206 Gln Thr Asn Thr Ile Ile Asp Val Gln Ile Ser Thr Pro Arg Pro Val
207 225          230          235          240
209 aaa tta ctt aga ggc cat act ctt gtc ctc aat tgt act gct acc act      768
210 Lys Leu Leu Arg Gly His Thr Leu Val Leu Asn Cys Thr Ala Thr Thr
211          245          250          255

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213	ccc	ttg	aac	acg	aga	gtt	caa	atg	acc	tgg	agt	tac	cct	gat	gaa	aaa	816
214	Pro	Leu	Asn	Thr	Arg	Val	Gln	Met	Thr	Trp	Ser	Tyr	Pro	Asp	Glu	Lys	
215				260					265				270				
217	aat	aag	aga	gct	tcc	gta	agg	cga	cga	att	gac	caa	agc	aat	tcc	cat	864
218	Asn	Lys	Arg	Ala	Ser	Val	Arg	Arg	Arg	Ile	Asp	Gln	Ser	Asn	Ser	His	
219			275				280					285					
221	gcc	aac	ata	ttc	tac	agt	gtt	ctt	act	att	gac	aaa	atg	cag	aac	aaa	912
222	Ala	Asn	Ile	Phe	Tyr	Ser	Val	Leu	Thr	Ile	Asp	Lys	Met	Gln	Asn	Lys	
223		290					295					300					
225	gac	aaa	gga	ctt	tat	act	tgt	cgt	gta	agg	agt	gga	cca	tca	ttc	aaa	960
226	Asp	Lys	Gly	Leu	Tyr	Thr	Cys	Arg	Val	Arg	Ser	Gly	Pro	Ser	Phe	Lys	
227	305					310					315					320	
229	tct	gtt	aac	acc	tca	gtg	cat	ata	tat	gat	aaa	gca	ggc	ccg	ggc	gag	1008
230	Ser	Val	Asn	Thr	Ser	Val	His	Ile	Tyr	Asp	Lys	Ala	Gly	Pro	Gly	Glu	
231				325					330						335		
233	ccc	aaa	tct	tgt	gac	aaa	act	cac	aca	tgc	cca	ccg	tgc	cca	gca	cct	1056
234	Pro	Lys	Ser	Cys	Asp	Lys	Thr	His	Thr	Cys	Pro	Pro	Cys	Pro	Ala	Pro	
235				340					345						350		
237	gaa	ctc	ctg	ggg	gga	ccg	tca	gtc	ttc	ctc	ttc	ccc	cca	aaa	ccc	aag	1104
238	Glu	Leu	Leu	Gly	Gly	Pro	Ser	Val	Phe	Leu	Phe	Pro	Pro	Lys	Pro	Lys	
239			355					360					365				
241	gac	acc	ctc	atg	atc	tcc	cgg	acc	cct	gag	gtc	aca	tgc	gtg	gtg	gtg	1152
242	Asp	Thr	Leu	Met	Ile	Ser	Arg	Thr	Pro	Glu	Val	Thr	Cys	Val	Val	Val	
243		370					375					380					
245	gac	gtg	agc	cac	gaa	gac	cct	gag	gtc	aag	ttc	aac	tgg	tac	gtg	gac	1200
246	Asp	Val	Ser	His	Glu	Asp	Pro	Glu	Val	Lys	Phe	Asn	Trp	Tyr	Val	Asp	
247	385					390					395					400	
249	ggc	gtg	gag	gtg	cat	aat	gcc	aag	aca	aag	ccg	cgg	gag	gag	cag	tac	1248
250	Gly	Val	Glu	Val	His	Asn	Ala	Lys	Thr	Lys	Pro	Arg	Glu	Glu	Gln	Tyr	
251				405					410						415		
253	aac	agc	acg	tac	cgt	gtg	gtc	agc	gtc	ctc	acc	gtc	ctg	cac	cag	gac	1296
254	Asn	Ser	Thr	Tyr	Arg	Val	Val	Ser	Val	Leu	Thr	Val	Leu	His	Gln	Asp	
255				420					425					430			
257	tgg	ctg	aat	ggc	aag	gag	tac	aag	tgc	aag	gtc	tcc	aac	aaa	gcc	ctc	1344
258	Trp	Leu	Asn	Gly	Lys	Glu	Tyr	Lys	Cys	Lys	Val	Ser	Asn	Lys	Ala	Leu	
259			435					440					445				
261	cca	gcc	ccc	atc	gag	aaa	acc	atc	tcc	aaa	gcc	aaa	ggg	cag	ccc	cga	1392
262	Pro	Ala	Pro	Ile	Glu	Lys	Thr	Ile	Ser	Lys	Ala	Lys	Gly	Gln	Pro	Arg	
263		450					455					460					
265	gaa	cca	cag	gtg	tac	acc	ctg	ccc	cca	tcc	cgg	gat	gag	ctg	acc	aag	1440
266	Glu	Pro	Gln	Val	Tyr	Thr	Leu	Pro	Pro	Ser	Arg	Asp	Glu	Leu	Thr	Lys	
267	465					470					475					480	
269	aac	cag	gtc	agc	ctg	acc	tgc	ctg	gtc	aaa	ggc	ttc	tat	ccc	agc	gac	1488
270	Asn	Gln	Val	Ser	Leu	Thr	Cys	Leu	Val	Lys	Gly	Phe	Tyr	Pro	Ser	Asp	
271				485					490						495		
273	atc	gcc	gtg	gag	tgg	gag	agc	aat	ggg	cag	ccg	gag	aac	aac	tac	aag	1536
274	Ile	Ala	Val	Glu	Trp	Glu	Ser	Asn	Gly	Gln	Pro	Glu	Asn	Asn	Tyr	Lys	
275				500					505						510		
277	acc	acg	cct	ccc	gtg	ctg	gac	tcc	gac	ggc	tcc	ttc	ttc	ctc	tac	agc	1584

RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/773,877

DATE: 08/07/2001

TIME: 08:23:37

Input Set : A:\REG 710B.txt

Output Set: N:\CRF3\08072001\I773877.raw

278 Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser
 279 515 520 525
 281 aag ctc acc gtg gac aag agc agg tgg cag cag ggg aac gtc ttc tca 1632
 282 Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser
 283 530 535 540
 285 tgc tcc gtg atg cat gag gct ctg cac aac cac tac acg cag aag agc 1680
 286 Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser
 287 545 550 555 560
 289 ctc tcc ctg tct ccg ggt aaa tga 1704
 290 Leu Ser Leu Ser Pro Gly Lys
 291 565
 294 <210> SEQ ID NO: 12
 295 <211> LENGTH: 567
 296 <212> TYPE: PRT
 C--> 297 <213> ORGANISM: Artificial
 W--> 299 <220> FEATURE:
 W--> 299 <223> OTHER INFORMATION: *Errored Field 223 requires a description of the artificial sequence named in field 213*
 299 <400> SEQUENCE: 12
 301 Met Val Ser Tyr Trp Asp Thr Gly Val Leu Leu Cys Ala Leu Leu Ser
 302 1 5 10 15
 305 Cys Leu Leu Leu Thr Gly Ser Ser Ser Gly Ser Lys Leu Lys Asp Pro
 306 20 25 30
 309 Glu Leu Ser Leu Lys Gly Thr Gln His Ile Met Gln Ala Gly Gln Thr
 310 35 40 45
 313 Leu His Leu Gln Cys Arg Gly Glu Ala Ala His Lys Trp Ser Leu Pro
 314 50 55 60
 317 Glu Met Val Ser Lys Glu Ser Glu Arg Leu Ser Ile Thr Lys Ser Ala
 318 65 70 75 80
 321 Cys Gly Arg Asn Gly Lys Gln Phe Cys Ser Thr Leu Thr Leu Asn Thr
 322 85 90 95
 325 Ala Gln Ala Asn His Thr Gly Phe Tyr Ser Cys Lys Tyr Leu Ala Val
 326 100 105 110
 329 Pro Thr Ser Lys Lys Lys Glu Thr Glu Ser Ala Ile Tyr Ile Phe Ile
 330 115 120 125
 333 Ser Asp Thr Gly Arg Pro Phe Val Glu Met Tyr Ser Glu Ile Pro Glu
 334 130 135 140
 337 Ile Ile His Met Thr Glu Gly Arg Glu Leu Val Ile Pro Cys Arg Val
 338 145 150 155 160
 341 Thr Ser Pro Asn Ile Thr Val Thr Leu Lys Lys Phe Pro Leu Asp Thr
 342 165 170 175
 345 Leu Ile Pro Asp Gly Lys Arg Ile Ile Trp Asp Ser Arg Lys Gly Phe
 346 180 185 190
 349 Ile Ile Ser Asn Ala Thr Tyr Lys Glu Ile Gly Leu Leu Thr Cys Glu
 350 195 200 205
 353 Ala Thr Val Asn Gly His Leu Tyr Lys Thr Asn Tyr Leu Thr His Arg
 354 210 215 220
 357 Gln Thr Asn Thr Ile Ile Asp Val Gln Ile Ser Thr Pro Arg Pro Val
 358 225 230 235 240
 361 Lys Leu Leu Arg Gly His Thr Leu Val Leu Asn Cys Thr Ala Thr Thr

The types of errors shown exist throughout the Sequence Listing. Please check subsequent sequences for similar errors.

VERIFICATION SUMMARY

PATENT APPLICATION: US/09/773,877

DATE: 08/07/2001

TIME: 08:23:38

Input Set : A:\REG 710B.txt

Output Set: N:\CRF3\08072001\I773877.raw

L:19 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:1
L:31 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:2
L:43 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:3
L:55 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:4
L:67 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:5
L:79 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:6
L:91 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:7
L:103 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:8
L:115 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:9
L:127 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:10
L:139 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:11
L:297 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:12
L:299 M:258 W: Mandatory Feature missing, <220> FEATURE:
L:299 M:258 W: Mandatory Feature missing, <223> OTHER INFORMATION:
L:448 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:13
L:602 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:14
L:604 M:258 W: Mandatory Feature missing, <220> FEATURE:
L:604 M:258 W: Mandatory Feature missing, <223> OTHER INFORMATION:
L:749 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:15
L:879 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:16
L:881 M:258 W: Mandatory Feature missing, <220> FEATURE:
L:881 M:258 W: Mandatory Feature missing, <223> OTHER INFORMATION:
L:1002 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:17
L:1132 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:18
L:1134 M:258 W: Mandatory Feature missing, <220> FEATURE:
L:1134 M:258 W: Mandatory Feature missing, <223> OTHER INFORMATION:
L:1255 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:19
L:1413 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:20
L:1415 M:258 W: Mandatory Feature missing, <220> FEATURE:
L:1415 M:258 W: Mandatory Feature missing, <223> OTHER INFORMATION:
L:1564 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:21
L:1696 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:22
L:1698 M:258 W: Mandatory Feature missing, <220> FEATURE:
L:1698 M:258 W: Mandatory Feature missing, <223> OTHER INFORMATION:
L:1819 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:23
L:1951 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:24
L:1953 M:258 W: Mandatory Feature missing, <220> FEATURE:
L:1953 M:258 W: Mandatory Feature missing, <223> OTHER INFORMATION:
L:2074 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:25
L:2204 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:26
L:2206 M:258 W: Mandatory Feature missing, <220> FEATURE:
L:2206 M:258 W: Mandatory Feature missing, <223> OTHER INFORMATION:
L:2327 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:27